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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/993,748	11/14/2001	Avi J. Ashkenazi	P2730P1C23	4944

35489 7590 03/09/2004

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EXAMINER	
LANDSMAN, ROBERT S	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 03/09/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/993,748	GENENTECH, INC.	
	Examiner	Art Unit	
	Robert Landsman	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *119-131* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *119-131* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *14 November 2001* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *5/24/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: Sequence Comparisons A-E

DETAILED ACTION

1. Formal Matters

A. The Preliminary Amendment dated 11/14/01, has been entered into the record.

B. Claims 119-131 are pending and are the subject of this Office Action.

2. Priority

Due to the excessive number of applications from which the present application claims benefit, priority cannot be determined. However, the Examiner has concluded that the subject matter defined in this application is not supported by any of the applications in the chain of priority because the presently claimed subject matter is not supported by a specific, substantial or well-established utility, nor, for this reason, is it enabled. Accordingly, the subject matter defined in claims 119-131 has an effective filing date of 11/14/01, which is the filing date of the present application.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 11/14/01 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 11/14/01.

3. Information Disclosure Statement

A. References A1 and A2 have been lined through since they are not in proper format, including author and date of deposit.

4. Specification

A. Though none could be found, due to the length of the specification, Applicants are reminded that embedded hyperlink and/or other form of browser-executable code are not permitted in the specification. See MPEP § 608.01.

B. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. The title recites polypeptides and polynucleotides whereas the claims are drawn to polypeptides.

5. Claim Objections

A. The syntax of claims 119-131 could be improved by replacing the phrase "shown in Figure 228 (SEQ ID NO:314)" with "of SEQ ID NO:314."

6. Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

A. Claims 119-131 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility. These claims are directed to polypeptides having various sequence homology to SEQ ID NO:314. However, the invention encompassed by these claims has no apparent or disclosed patentable utility. This rejection is consistent with the current utility guidelines, published 1/5/01, 66 FR 1092. The instant application has provided a description of an isolated protein. However, the instant application does not disclose a specific and substantial biological role of this protein or its significance.

However, it is clear from the instant specification that the claimed protein is what is termed an "orphan receptor" in the art. The instant application does not disclose the biological role of the claimed protein or its significance. Applicants disclose in the specification that the receptor has certain amino acid sequence identity with microfibril-associated glycoprotein 4 (MFA4 HUMAN); ficolin-A - Mus musculus (M0078131); human lectin P35 (D63155561); ficolin B - Mus musculus (AF00632171); human tenascin-R (restriction) (HS518E13 1); the long form of a rat janusin precursor (A45445); fibrinogen-related protein HFREP-I precursor (JNO596); a human Tenascin precursor (TENA HUMAN); hllman CDT6 (HSY16132 1); and angiopoietin-l - Mus musculus (MM1.183509 1). Therefore, Applicants believe that NL7 disclosed the present application is a novel TIE ligand homologue, and may play a role in angiogenesis and/or vascular maintenance and/or wound healing and/or inflammation and/or tumor development and/or growth. However, homology alone is not sufficient to demonstrate utility of the present invention. There is little doubt that, after complete characterization, this protein will probably be found to have a patentable utility. This further characterization, however, is part of the act of invention and, until it has been undertaken, Applicants' claimed invention is incomplete.

The instant situation is directly analogous to that of which was addressed in Brenner v. Manson, 148 U.S.P.Q. 689 (Sus. Ct, 1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anticancer activity was alleged to be potentially useful as an

antitumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. 101, which required that an invention must have either an immediate obvious or fully disclosed "real-world" utility. The court held that:

> "The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility," "[u]nless and until a process is refined and developed to this point - where specific benefit exists in currently available form – there is insufficient justification for permitting an applicant to engross what may prove to be a broad field," and "a patent is not a hunting license," "[i]t is not a reward for the search, but compensation for its successful conclusion."

The specification discloses that the polynucleotides of the invention encode proteins which have significant sequence similarity to known proteins. Based on the structural similarity, the specification asserts that the newly disclosed SEQ ID NO:314 has similar activities. The assertion that the disclosed proteins have biological activities similar to known proteins cannot be accepted in the absence of supporting evidence, because generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene.

Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign

functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts.

Therefore, based on the discussions above concerning the specific examples of structurally similar proteins that have different functions, along with the art's recognition that one cannot rely upon structural similarity alone to determine functionality, the specification fails to teach the skilled artisan the utility of the protein of SEQ ID NO:314 which is only known to be homologous to various receptors. Therefore, the instant claims are drawn to a polynucleotide encoding a protein which has a yet undetermined function or biological significance. There is no actual and specific significance which can be attributed to said protein identified in the specification. For this reason, the instant invention is incomplete. In the absence of a knowledge of the natural ligands or biological significance of this protein, there is no immediately obvious patentable use for it. To employ a protein of the instant invention in the identification of substances which bind to and/or mediate activity of the said receptor is clearly to use it as the object of further research which has been determined by the courts to be a non-patentable utility. Since the instant specification does not disclose a "real-world" use for said protein then the claimed invention is incomplete and, therefore, does not meet the requirements of 35 U.S.C. 101 as being useful.

Furthermore, since the protein of the invention is not supported by a specific and substantial asserted utility or a well established utility, the encoding polynucleotides and chimeric proteins also lack utility.

7. Claim Rejections - 35 USC § 112, first paragraph - enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A. Claims 119-131 are rejected under 35 U.S.C. 112, first paragraph, as failing to adequately teach how to use the instant invention. Specifically, since the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

B. Claims 119-131 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The deposit of the biological material is considered necessary for the enablement of the current invention (see MPEP Chapter 2400 and 37 C.F.R. §§ 1.801-1.809). Elements required for practicing a claimed invention must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If a deposit (203128) is made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure (e.g. see 961 OG 21, 1977), and Applicants, their assignee or their agent needs to provide a declaration containing the following:

1. the current address of the ATCC.
2. a declaration, or statement over attorney's signature stating that all restrictions imposed by the depositor on the availability to the public of the deposited biological material be irrevocably removed upon the granting of the patent (see MPEP Chapter 2410.01 and 37 C.F.R. § 1.808.

C. Furthermore, even if the claims possessed utility under 35 USC 101, claims 119-131 would still be rejected under 35 USC 112, first paragraph, because the specification, while then being enabling for SEQ ID NO:313 and 314, does not reasonably provide enablement for polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity to SEQ ID NO:314, to the protein encoded by ATCC No. 203128, for the extracellular domain thereof, or for fusion proteins. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. There is no functional limitation in the claims. The claims encompass an unreasonable number of inoperative polypeptides, or polynucleotides which encode these polypeptides, which the skilled artisan would not know how to use.

There are no working examples of polynucleotides or polypeptides less than 100% identical to SEQ ID NO:313 or 314, or the mature form thereof (i.e. lacking its signal peptide). The skilled artisan would not know how to use non-identical polypeptides on the basis of teachings in the prior art or specification unless they possessed a specific function disclosed in the instant specification, in which there is none. While the specification generally describes homologous proteins, Applicants still have not taught to which family of proteins the protein of the present invention belongs. The specification does not provide guidance for using polynucleotides encoding polypeptides related to (*i.e.,* 80%-99% identity) but not identical to SEQ ID NO:313 or 314 which do not have any specific, known function. The claims are broad because they do not require the claimed polypeptide to be identical to the disclosed sequence and because the claims have no functional limitation.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of proteases and lack of knowledge about function(s) of encompassed polypeptides structurally related to SEQ ID NO:314, the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:314, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

8. Claim Rejections - 35 USC § 112, first paragraph – written description

A. Claims 119-131 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity with SEQ ID NO:314, and fusion proteins thereof. The claims do not require that the polypeptide of the present invention possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless

of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO:314, or encoded by SEQ ID NO:313, but not the full breadth of the claims, meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

9. Claim Rejections - 35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 119-131 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. Claims 119-131 are vague and indefinite since it is not clear whether or not the protein of the present invention is a soluble protein (e.g protease), nor is it disclosed as being expressed on a cell surface. Accordingly, the limitation that the claimed protein comprises an "extracellular domain" is indefinite, as the art does not recognize soluble proteins as having such domains. Further, if the protein had an extracellular domain, the recitation of "the extracellular domain"..."lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

10. Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

A. Claims 119-131 are rejected under 35 U.S.C. 102(b) as being anticipated by Baker et al. (WO 99/63088). The claims recite an isolated polypeptide at least 80% identical to SEQ ID NO:314 as well as polynucleotides encoding this protein, extracellular domains and chimeric polypeptides. Baker et al. teach a protein which is 100% identical to SEQ ID NO:314 of the present invention (Sequence Comparison A and B). This protein would encompass all of the claimed variants of that of the present invention. Baker also teach chimeric peptides (page 350, line 15).

11. Art of Interest

A. Fernandez et al. teach a protein which is 60.5% identical to that of SEQ ID NO:314 of the present invention (Sequence Comparison C).

12. Conclusion

A. No claim is allowable.

Advisory information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Robert Landsman whose telephone number is (703) 306-3407. The examiner can normally be reached on Monday - Friday from 8:00 AM to 5:00 PM (Eastern time) and alternate Fridays from 8:00 AM to 5:00 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the Examiner's supervisor, Gary Kunz, can be reached on (703) 308-4623.

Official papers filed by fax should be directed to (703) 308-4242. Fax draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Robert Landsman, Ph.D.
Patent Examiner
Group 1600
March 05, 2004

ROBERT LANDSMAN
PATENT EXAMINER

Sequence Comparison A

```
ID   AAY66727 standard; protein; 461 AA.
XX
DT   05-APR-2000  (first entry)
XX
DE   Membrane-bound protein PRO1346.
XX
KW   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW   pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
PF   02-JUN-1999;   99WO-US12252.
XX
PR   02-JUN-1998;   98US-0087607.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Chen J,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK;
PI   Wood WI,  Yuan J;
XX
DR   WPI; 2000-072883/06.
DR   N-PSDB; AAZ65071.
XX
PT   Membrane-bound proteins and related nucleotide sequences  -
XX
PS   claim 12; Fig 228; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC   will also be useful for the preparation of PRO polypeptides, especially
CC   by recombinant techniques.
XX
SQ   Sequence   461 AA;

  Query Match             100.0%;  Score 2450;  DB 21;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-225;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAP 60

Qy         61 GTAPPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTAPPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALT 120

Qy        121 EHQAQPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EHQAQPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQG 180
```

Sequence Comparism
A cont'd

```
Qy        181 RLIQLLSESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLIQLLSESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSR 240

Qy        241 PRDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PRDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWD 300

Qy        301 AYRDGFGRLTGEHWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AYRDGFGRLTGEHWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPE 360

Qy        361 EDGYPLTVADYSGTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EDGYPLTVADYSGTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLN 420

Qy        421 GQYLRGAHASYADGVEWSSWTGWQYSLKFSEMKIRPVREDR 461
              |||||||||||||||||||||||||||||||||||||||||
Db        421 GQYLRGAHASYADGVEWSSWTGWQYSLKFSEMKIRPVREDR 461
```

Sequence Comparism
B

```
ID   AAZ65071 standard; cDNA; 3010 BP.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
SQ   Sequence 3010 BP; 497 A; 1045 C; 938 G; 530 T; 0 other;
```

Alignment Scores:

Pred. No.:	1.09e-191	Length:	3010
Score:	2450.00	Matches:	461
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-989-729A-314 (1-461) x AAZ65071 (1-3010)

```
Qy          1 MetValAsnAspArgTrpLysThrMetGlyGlyAlaAlaGlnLeuGluAspArgProArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGC 60

Qy         21 AspLysProGlnArgProSerCysGlyTyrValLeuCysThrValLeuLeuAlaLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCT 120

Qy         41 ValLeuLeuAlaValAlaValThrGlyAlaValLeuPheLeuAsnHisAlaHisAlaPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTGCTGGCTGTAGCTGTCACCGGTGCCGTGCTCTTCCTGAACCACGCCCACGCGCCG 180

Qy         61 GlyThrAlaProProProValValSerThrGlyAlaAlaSerAlaAsnSerAlaLeuVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCACGGCGCCCCCACCTGTCGTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTC 240

Qy         81 ThrValGluArgAlaAspSerSerHisLeuSerIleLeuIleAspProArgCysProAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGTGGAAAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGAC 300
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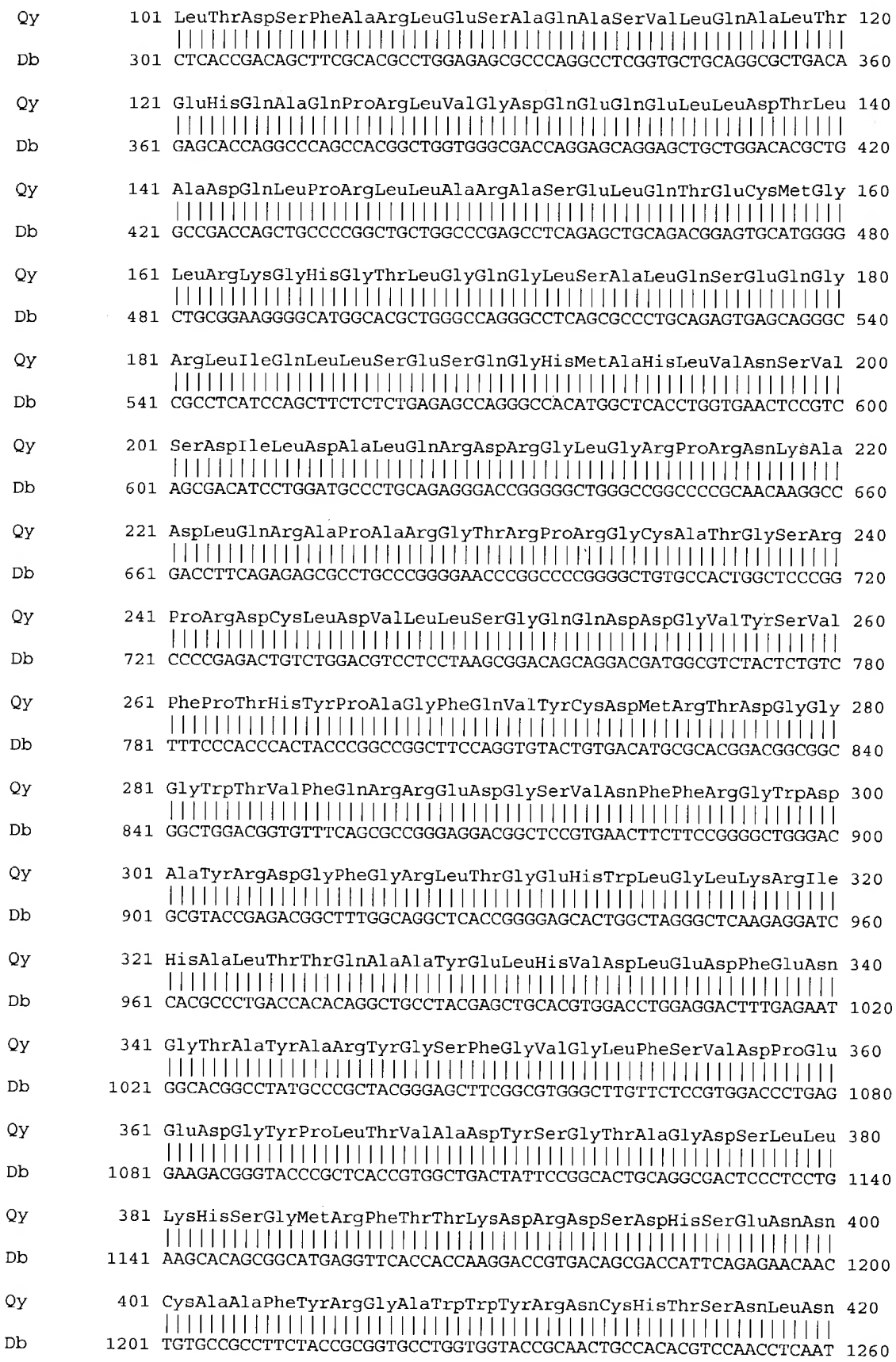
B cont'd


Qy 101 LeuThrAspSerPheAlaArgLeuGluSerAlaGlnAlaSerValLeuGlnAlaLeuThr 120
Db 301 CTCACCGACAGCTTCGCACGCCTGGAGAGCGCCCAGGCCTCGGTGCTGCAGGCGCTGACA 360
Qy 121 GluHisGlnAlaGlnProArgLeuValGlyAspGlnGluGlnGluLeuLeuAspThrLeu 140
Db 361 GAGCACCAGGCCCAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTG 420
Qy 141 AlaAspGlnLeuProArgLeuLeuAlaArgAlaSerGluLeuGlnThrGluCysMetGly 160
Db 421 GCCGACCAGCTGCCCCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGG 480
Qy 161 LeuArgLysGlyHisGlyThrLeuGlyGlnGlyLeuSerAlaLeuGlnSerGluGlnGly 180
Db 481 CTGCGGAAGGGGCATGGCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGC 540
Qy 181 ArgLeuIleGlnLeuLeuSerGluSerGlnGlyHisMetAlaHisLeuValAsnSerVal 200
Db 541 CGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACTCCGTC 600
Qy 201 SerAspIleLeuAspAlaLeuGlnArgAspArgGlyLeuGlyArgProArgAsnLysAla 220
Db 601 AGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCC 660
Qy 221 AspLeuGlnArgAlaProAlaArgGlyThrArgProArgGlyCysAlaThrGlySerArg 240
Db 661 GACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGG 720
Qy 241 ProArgAspCysLeuAspValLeuLeuSerGlyGlnGlnAspAspGlyValTyrSerVal 260
Db 721 CCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTC 780
Qy 261 PheProThrHisTyrProAlaGlyPheGlnValTyrCysAspMetArgThrAspGlyGly 280
Db 781 TTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTGACATGCGCACGGACGGCGGC 840
Qy 281 GlyTrpThrValPheGlnArgArgGluAspGlySerValAsnPhePheArgGlyTrpAsp 300
Db 841 GGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGAC 900
Qy 301 AlaTyrArgAspGlyPheGlyArgLeuThrGlyGluHisTrpLeuGlyLeuLysArgIle 320
Db 901 GCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCTAGGGCTCAAGAGGATC 960
Qy 321 HisAlaLeuThrThrGlnAlaAlaTyrGluLeuHisValAspLeuGluAspPheGluAsn 340
Db 961 CACGCCCTGACCACACAGGCTGCCTACGAGCTGCACGTGGACCTGGAGGACTTTGAGAAT 1020
Qy 341 GlyThrAlaTyrAlaArgTyrGlySerPheGlyValGlyLeuPheSerValAspProGlu 360
Db 1021 GGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTGTTCTCCGTGGACCCTGAG 1080
Qy 361 GluAspGlyTyrProLeuThrValAlaAspTyrSerGlyThrAlaGlyAspSerLeuLeu 380
Db 1081 GAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGCAGGCGACTCCCTCCTG 1140
Qy 381 LysHisSerGlyMetArgPheThrThrLysAspArgAspSerAspHisSerGluAsnAsn 400
Db 1141 AAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGCGACCATTCAGAGAACAAC 1200
Qy 401 CysAlaAlaPheTyrArgGlyAlaTrpTrpTyrArgAsnCysHisThrSerAsnLeuAsn 420
Db 1201 TGTGCCGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAAT 1260

B cont'd

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Qy        421 GlyGlnTyrLeuArgGlyAlaHisAlaSerTyrAlaAspGlyValGluTrpSerSerTrp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGTGGAGTGGTCCTCCTGG 1320

Qy        441 ThrGlyTrpGlnTyrSerLeuLysPheSerGluMetLysIleArgProValArgGluAsp 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCGGCCGGTCCGGGAGGAC 1380

Qy        461 Arg 461
              |||
Db       1381 CGC 1383
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Sequence Comparison B

C

ID AAB19732 standard; Protein; 269 AA.
XX
AC AAB19732;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human SECX Clone 4437909.0.4 encoded protein.
XX
KW SECX; human; diagnosis; therapy; reproductive disorder;
KW muscular disorder; immunological disorder; cancer; infection.
XX
OS Homo sapiens.
XX
PN WO200061754-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US09392.
XX
PR 09-APR-1999; 99US-0128514.
PR 03-MAR-2000; 2000US-0128514.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Fernandez E, Vernet C, Shimkets R;
XX
DR WPI; 2000-679487/66.
DR N-PSDB; AAA88801.
XX
PT SECX polypeptides and the nucleic acids that encode them, useful for
PT diagnosing, preventing and treating e.g. cancers, inflammation,
PT arthritis and immunological disorders -
XX
PS Claim 1; Fig 13; 143pp; English.
XX
CC The present sequence is that of the protein encoded by novel SECX
CC Clone 4437909.0.4 (see AAA88801). It is a microbody (peroxisome)
CC associated protein expressed in osteogenic sarcoma cell lines,
CC adrenal gland, thalamus, foetal brain and foetal lung. The
CC invention provides novel SECX polynucleotides (see AAA88789-804) and
CC the secreted or membrane-associated proteins encoded by them (see
CC AAB19720-34). SECX polynucleotides, polypeptides and antibodies can
CC be used in the detection, diagnosis and treatment (including gene
CC therapy) of a broad range of pathological states. 4437909.0.4
CC protein shows similarity to human microfibril-associated glycoprotein
CC 4 splice variant MAG4V and may therefore be useful for treating
CC reproductive disorders (e.g. disruptions of the oestrus cycle and
CC spermatogenesis, polycystic ovary syndrome and cancers of the
CC prostate and ovary), muscular disorders (e.g. Duchenne's muscular
CC dystrophy, lipid myopathy and myocarditis), immunological
CC disorders (e.g. Addison's disease, asthma, anaemia and AIDS) and
CC neoplastic disorders (e.g. myeloma, sarcoma, leukaemia and lung
CC cancer). Similarity is also shown to human opsonin protein P35,
CC suggesting use in the prevention and treatment of infectious
CC diseases. A variant of 4437909.0.4 is given in AAB19733.
XX
SQ Sequence 269 AA;

C cont'd

Query Match 60.5%; Score 1483; DB 21; Length 269;
Best Local Similarity 100.0%; Pred. No. 6.1e-133;
Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      193 MAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVLLSGQ 252
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVLLSGQ 60

Qy      253 QDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLTGE 312
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 QDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLTGE 120

Qy      313 HWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPEEDGYPLTVADYS 372
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 HWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPEEDGYPLTVADYS 180

Qy      373 GTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYA 432
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASYA 240

Qy      433 DGVEWSSWTGWQYSLKFSEMKIRPVREDR 461
            |||||||||||||||||||||||||||||
Db      241 DGVEWSSWTGWQYSLKFSEMKIRPVREDR 269
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